

Input Set: I552705.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Chen, Shiuan
2 Zhou, Dujin
3 <120> TITLE OF INVENTION: DRUG SCREENING USING A PROLINE-RICH NUCLEAR RECEPTOR
4 CO-REGULATORY PROTEIN/NUCLEAR RECEPTOR CO-EXPRESSION
5 SYSTEM
6 <130> FILE REFERENCE: 2124-311
7 <140> CURRENT APPLICATION NUMBER: US/09/552,705
8 <141> CURRENT FILING DATE: 2000-04-19
9 <150> EARLIER APPLICATION NUMBER: U.S. 60/129,873
10 <151> EARLIER FILING DATE: 1999-04-19
11 <160> NUMBER OF SEQ ID NOS: 9
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 30
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial Sequence
17 <220> FEATURE:
18 <223> OTHER INFORMATION: Description of Artificial Sequence: Sense primer.
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22 <211> LENGTH: 39
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Artificial Sequence: Antisense
27 primer.
28 <400> SEQUENCE: 2
29 ggcgtcgacg gatcctcaga ctgtggcagg gaaaccctc 39
30 <210> SEQ ID NO 3
31 <211> LENGTH: 12
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
34 <400> SEQUENCE: 3
35 ccaaggtcag aa 12
36 <210> SEQ ID NO 4
37 <211> LENGTH: 5
38 <212> TYPE: PRT
39 <213> ORGANISM: Homo sapiens
40 <400> SEQUENCE: 4
41 Leu Lys Thr Leu Leu
42 1 5
43 <210> SEQ ID NO 5
44 <211> LENGTH: 7

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45 <212> TYPE: PRT
46 <213> ORGANISM: Homo sapiens
47 <400> SEQUENCE: 5
48   Ser Asp Pro Pro Ser Pro Ser
49       1               5
50 <210> SEQ ID NO 6
51 <211> LENGTH: 7
52 <212> TYPE: PRT
53 <213> ORGANISM: Homo sapiens
54 <220> FEATURE:
55 <221> NAME/KEY: MUTAGEN
56 <222> LOCATION: (3)
57 <223> OTHER INFORMATION: This residue has been changed from a proline.
58 <220> FEATURE:
59 <221> NAME/KEY: MUTAGEN
60 <222> LOCATION: (6)
61 <223> OTHER INFORMATION: This residue has been changed from a proline.
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64       1               5
65 <210> SEQ ID NO 7
66 <211> LENGTH: 2061
67 <212> TYPE: DNA
68 <213> ORGANISM: Homo sapiens
69 <220> FEATURE:
70 <221> NAME/KEY: CDS
71 <222> LOCATION: (114)..(1094)
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73   tgttccgcga tcttctcagg ctctcctagc agcatccatc gccgccaccc tatcttcact 60
74   ggcttcacct tctccttctc tcttcgttgc tgagcgacaa gcttcctagc gct atg 116
75                                     Met
76                                     1
77   act gtc gtc tcc gtc ccg cag cgg gag ccg ctc gtc ctg ggt ggc cgc 164
78   Thr Val Val Ser Val Pro Gln Arg Glu Pro Leu Val Leu Gly Gly Arg
79               5               10               15
80   ctt gcg ccg ctt ggc ttt tcc tcc cga ggt tac ttt ggg gcc ctc ccg 212
81   Leu Ala Pro Leu Gly Phe Ser Ser Arg Gly Tyr Phe Gly Ala Leu Pro
82       20               25               30
83   atg gtg acc acg gct ccg cct cct tta ccc cgg atc ccg gac ccc cgg 260
84   Met Val Thr Thr Ala Pro Pro Pro Leu Pro Arg Ile Pro Asp Pro Arg
85       35               40               45
86   gca ctg ccc ccg acc ctc ttc ctc cct cat ttc cta ggg gga gat ggc 308
87   Ala Leu Pro Pro Thr Leu Phe Leu Pro His Phe Leu Gly Gly Asp Gly
88       50               55               60               65
89   ccg tgt ctg acc ccc cag cct cgc gct cca gca gct ctg ccc aac cgc 356
90   Pro Cys Leu Thr Pro Gln Pro Arg Ala Pro Ala Ala Leu Pro Asn Arg
91               70               75               80
92   agc ctc gcc gtg gcg gga ggc act cct cgg gca gcg ccg aag aag cgg 404
93   Ser Leu Ala Val Ala Gly Gly Thr Pro Arg Ala Ala Pro Lys Lys Arg
94               85               90               95

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95	cga aag aag aag gtg cgg gcc agc ccc gca ggg cag ctg ccc agc cgc	452
96	Arg Lys Lys Lys Val Arg Ala Ser Pro Ala Gly Gln Leu Pro Ser Arg	
97	100 105 110	
98	ttc cac cag tac cag cag cac cgg ccg agt ctg gag ggc ggc cgg agc	500
99	Phe His Gln Tyr Gln Gln His Arg Pro Ser Leu Glu Gly Gly Arg Ser	
100	115 120 125	
101	ccc gcg acc ggc ccg agc gga gcg cag gag gtc ccg ggc ccg gcc gcc	548
102	Pro Ala Thr Gly Pro Ser Gly Ala Gln Glu Val Pro Gly Pro Ala Ala	
103	130 135 140 145	
104	gcc ttg gcc ccg agt cct gca gcc gca gcc ggc acg gag gga gcc agc	596
105	Ala Leu Ala Pro Ser Pro Ala Ala Ala Gly Thr Glu Gly Ala Ser	
106	150 155 160	
107	ccc gac ctt gcc ccg ctg cgg ccc gcg gct ccc ggc caa acc ccc ctc	644
108	Pro Asp Leu Ala Pro Leu Arg Pro Ala Ala Pro Gly Gln Thr Pro Leu	
109	165 170 175	
110	agg aaa gag gtt tta aaa tca aag atg gga aaa tcg gag aaa att gcc	692
111	Arg Lys Glu Val Leu Lys Ser Lys Met Gly Lys Ser Glu Lys Ile Ala	
112	180 185 190	
113	ctt ccc cat ggc cag ctt gtt cat ggt ata cac ttg tat gag caa cca	740
114	Leu Pro His Gly Gln Leu Val His Gly Ile His Leu Tyr Glu Gln Pro	
115	195 200 205	
116	aag ata aac aga cag aaa agc aaa tat aac ttg cca cta acc aag atc	788
117	Lys Ile Asn Arg Gln Lys Ser Lys Tyr Asn Leu Pro Leu Thr Lys Ile	
118	210 215 220 225	
119	acc tct gca aaa aga aat gaa aac aac ttt tgg cag gat tct gtt tca	836
120	Thr Ser Ala Lys Arg Asn Glu Asn Asn Phe Trp Gln Asp Ser Val Ser	
121	230 235 240	
122	tct gac aga att cag aag cag gaa aaa aag cct ttt aaa aat acc gag	884
123	Ser Asp Arg Ile Gln Lys Gln Glu Lys Lys Pro Phe Lys Asn Thr Glu	
124	245 250 255	
125	aac att aaa aat tcg cat ttg aag aaa tca gca ttt cta act gaa gtg	932
126	Asn Ile Lys Asn Ser His Leu Lys Lys Ser Ala Phe Leu Thr Glu Val	
127	260 265 270	
128	agc caa aag gaa aat tat gct ggg gca aag ttt agt gat cca cct tct	980
129	Ser Gln Lys Glu Asn Tyr Ala Gly Ala Lys Phe Ser Asp Pro Pro Ser	
130	275 280 285	
131	cct agt gtt ctt cca aag cct cct agt cac tgg atg gga agc act gtt	1028
132	Pro Ser Val Leu Pro Lys Pro Pro Ser His Trp Met Gly Ser Thr Val	
133	290 295 300 305	
134	gaa aat tcc aac caa aac agg gag ctg atg gca gta cac tta aaa acc	1076
135	Glu Asn Ser Asn Gln Asn Arg Glu Leu Met Ala Val His Leu Lys Thr	
136	310 315 320	
137	ctc ctc aaa gtt caa act tagatttcag atttcagtat gtgtgtaaaa	1124
138	Leu Leu Lys Val Gln Thr	
139	325	
140	cataattttt cccatatccc tggactcttg agaaaattgg tacagaaatg gaaatttgcc	1184
141	ttgttgcaac atacaattgc aaaagatgag tttaaaaaat tacatacaaa cagcttgtat	1244
142	tatatatttat attttgtaaa tactgtatac catgtattat gtgtatatattg ttcatacttg	1304
143	agagggtatat tatagttttg ttatgaaagt atgtattttg ccctgccac attgcagggtg	1364
144	ttttgtatat atacaatgga taaattttta gtgtgtgcta aggcacatgg aagaccgatt	1424

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145      ttatttgcac aaggctactga gatttttttc aagaaacagc tgtcaaactct caagggtgaag 1484
146      atctaaatgt gaacagttta ctaatgcact actgaagttt aaatctgtgg cacaatcaat 1544
147      gtaagcatgg ggtttgtttc tctaaattga tttgtaactct gaaattactg aacaactcct 1604
148      attccatttt ttgctaaact caatttctgg ttttggtata tatccattcc agcttaatgc 1664
149      ctctaatttt aatgccaaaca aaattgggtg taatcaaatt ttaaaataat aataatttgg 1724
150      cccccctttt taaaatagtc ttgactcttt gtgtgtgact gtttctcatg tttgaatgtg 1784
151      tgactaggag atgatattgt gtggttggat ttttttgact tctactttac tggctgagtg 1844
152      tgagccgcca tgcctggcca taatctacat tttcttacca ggagcagcat tgagggtttt 1904
153      gagcatagta cttgactact ctagaggctg agacgggagc atctcttgag cctgagaagt 1964
154      ggagattgca attgagctag gatcaggcca ctgcactcca gcctgggtaa cagacgctgt 2024
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156 <210> SEQ ID NO 8

157 <211> LENGTH: 327

158 <212> TYPE: PRT

159 <213> ORGANISM: Homo sapiens

160 <400> SEQUENCE: 8

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163      Arg Leu Ala Pro Leu Gly Phe Ser Ser Arg Gly Tyr Phe Gly Ala Leu
164      20          25          30
165      Pro Met Val Thr Thr Ala Pro Pro Leu Pro Arg Ile Pro Asp Pro
166      35          40          45
167      Arg Ala Leu Pro Pro Thr Leu Phe Leu Pro His Phe Leu Gly Gly Asp
168      50          55          60
169      Gly Pro Cys Leu Thr Pro Gln Pro Arg Ala Pro Ala Ala Leu Pro Asn
170      65          70          75          80
171      Arg Ser Leu Ala Val Ala Gly Gly Thr Pro Arg Ala Ala Pro Lys Lys
172      85          90          95
173      Arg Arg Lys Lys Lys Val Arg Ala Ser Pro Ala Gly Gln Leu Pro Ser
174      100         105         110
175      Arg Phe His Gln Tyr Gln Gln His Arg Pro Ser Leu Glu Gly Gly Arg
176      115         120         125
177      Ser Pro Ala Thr Gly Pro Ser Gly Ala Gln Glu Val Pro Gly Pro Ala
178      130         135         140
179      Ala Ala Leu Ala Pro Ser Pro Ala Ala Ala Ala Gly Thr Glu Gly Ala
180      145         150         155         160
181      Ser Pro Asp Leu Ala Pro Leu Arg Pro Ala Ala Pro Gly Gln Thr Pro
182      165         170         175
183      Leu Arg Lys Glu Val Leu Lys Ser Lys Met Gly Lys Ser Glu Lys Ile
184      180         185         190
185      Ala Leu Pro His Gly Gln Leu Val His Gly Ile His Leu Tyr Glu Gln
186      195         200         205
187      Pro Lys Ile Asn Arg Gln Lys Ser Lys Tyr Asn Leu Pro Leu Thr Lys
188      210         215         220
189      Ile Thr Ser Ala Lys Arg Asn Glu Asn Asn Phe Trp Gln Asp Ser Val
190      225         230         235         240
191      Ser Ser Asp Arg Ile Gln Lys Gln Glu Lys Lys Pro Phe Lys Asn Thr
192      245         250         255
193      Glu Asn Ile Lys Asn Ser His Leu Lys Lys Ser Ala Phe Leu Thr Glu
194      260         265         270

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195      Val Ser Gln Lys Glu Asn Tyr Ala Gly Ala Lys Phe Ser Asp Pro Pro
196              275                      280                      285
197      Ser Pro Ser Val Leu Pro Lys Pro Pro Ser His Trp Met Gly Ser Thr
198              290                      295                      300
199      Val Glu Asn Ser Asn Gln Asn Arg Glu Leu Met Ala Val His Leu Lys
200      305                      310                      315                      320
201      Thr Leu Leu Lys Val Gln Thr
202              325
203      <210> SEQ ID NO 9
204      <211> LENGTH: 23
205      <212> TYPE: PRT
206      <213> ORGANISM: Homo sapiens
207      <400> SEQUENCE: 9
208      Asn Tyr Ala Gly Ala Lys Phe Ser Asp Pro Pro Ser Pro Ser Val Leu
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210      Pro Lys Pro Pro Ser His Trp
211              20

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
